

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/357,709

DATE: 03/29/2001
 TIME: 16:20:44

Input Set : A:\242-026.txt
 Output Set: N:\CRF3\03292001\I357709.raw

#8 1/2
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3 <110> APPLICANT: Bander, Neil H.
 5 <120> TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
 7 <130> FILE REFERENCE: Lois M. Kwasigroch: BZL 242/026
 9 <140> CURRENT APPLICATION NUMBER: US 09/357,709
 10 <141> CURRENT FILING DATE: 1999-07-20
 12 <150> PRIOR APPLICATION NUMBER: US 08/838,682
 13 <151> PRIOR FILING DATE: 1997-04-09
 15 <150> PRIOR APPLICATION NUMBER: US 60/016,976
 16 <151> PRIOR FILING DATE: 1996-05-06
 18 <150> PRIOR APPLICATION NUMBER: US 60/022,125
 19 <151> PRIOR FILING DATE: 1996-07-18
 21 <160> NUMBER OF SEQ ID NOS: 21
 23 <170> SOFTWARE: PatentIn version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 391
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Mus sp.
 30 <400> SEQUENCE: 1
 31 tctcctgtca ggaactgcag gtgtcctctc tgaggtccag ctgcaacagt ctggacctga 60
 33 actggtgaag cctgggactt cagtggaggat atcctgcaag acttctggat acacattcac 120
 35 tgaatatacc atacactggg tgaagcagag ccatggaaag agccttgagt ggattggaaa 180
 37 catcaatcct aacaatgggt gtaccaccta caatcagaag ttcgaggaca aggccacatt 240
 39 gactgtagac aagtcctcca gtacagccta catggagctc cgcagcctaa catctgagga 300
 41 ttctgcagtc tattattgtg cagctggttg gaactttgac tactggggcc aaggcaccac 360
 43 tctcacagtc tctcagcca aaacgacacc c 391
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 47 <211> LENGTH: 391
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Mus sp.
 51 <400> SEQUENCE: 2
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 54 ccaaccagct gcacaataat agactgcaga atcctcagat gttaggctgc ggagctccat 120
 56 gtaggctgta ctggaggact tgtctacagt caatgtggcc ttgtcctcga acttctgatt 180
 58 gtaggtggtg ccaccattgt taggattgat gtttccaatc cactcaaggc tctttccatg 240
 60 gctctgcttc acccagtgta tggatatatt agtgaatgtg tatccagaag tcttgacagga 300
 62 tctcctcact gaagtcccag gcttcaccag ttcaggtoca gactgttgca gctggacctc 360
 64 agagaggaca cctgcagttc ctagcaggag a 391
 67 <210> SEQ ID NO: 3
 68 <211> LENGTH: 123
 69 <212> TYPE: PRT
 70 <213> ORGANISM: Mus sp.
 72 <400> SEQUENCE: 3
 74 Ser Pro Val Arg Asn Cys Arg Cys Pro Leu Gly Pro Ala Ala Thr Val
 75 1 5 10 15
 77 Trp Thr Thr Gly Glu Ala Trp Asp Phe Ser Glu Asp Ile Leu Gln Asp
 78 20 25 30
 80 Phe Trp Ile His Ile His Ile Tyr His Thr Leu Gly Glu Ala Glu Pro

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81      35      40      45
83 Trp Lys Glu Pro Val Asp Trp Lys His Gln Ser Gln Trp Trp Tyr His
84      50      55      60
86 Leu Gln Ser Glu Val Arg Gly Gln Gly His Ile Asp Cys Arg Gln Val
87 65      70      75      80
89 Leu Gln Tyr Ser Leu His Gly Ala Pro Gln Pro Asn Ile Gly Phe Cys
90      85      90      95
92 Ser Leu Leu Leu Cys Ser Trp Leu Glu Leu Leu Leu Gly Pro Arg His
93      100      105      110
95 His Ser His Ser Leu Leu Ser Gln Asn Asp Thr
96      115      120
98 <210> SEQ ID NO: 4
99 <211> LENGTH: 130
100 <212> TYPE: PRT
101 <213> ORGANISM: Mus sp.
103 <400> SEQUENCE: 4
105 Leu Leu Ser Gly Thr Ala Gly Val Leu Ser Glu Val Gln Leu Gln Gln
106 1      5      10      15
108 Ser Gly Pro Glu Leu Val Lys Pro Gly Thr Ser Val Arg Ile Ser Cys
109      20      25      30
111 Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr Thr Ile His Trp Val Lys
112      35      40      45
114 Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Asn Ile Asn Pro Asn
115      50      55      60
117 Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe Glu Asp Lys Ala Thr Leu
118 65      70      75      80
120 Thr Val Asp Lys Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu
121      85      90      95
123 Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Ala Gly Trp Asn Phe
124      100      105      110
126 Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr
127      115      120      125
129 Thr Pro
130      130
132 <210> SEQ ID NO: 5
133 <211> LENGTH: 125
134 <212> TYPE: PRT
135 <213> ORGANISM: Mus sp.
137 <400> SEQUENCE: 5
139 Leu Ser Cys Gln Glu Leu Gln Val Ser Ser Leu Arg Ser Ser Cys Asn
140 1      5      10      15
142 Ser Leu Asp Leu Asn Trp Ser Leu Gly Leu Gln Gly Tyr Pro Ala Arg
143      20      25      30
145 Leu Leu Asp Thr His Ser Leu Asn Ile Pro Tyr Thr Gly Ser Arg Ala
146      35      40      45
148 Met Glu Arg Ala Leu Ser Gly Leu Glu Thr Ser Ile Leu Thr Met Val
149      50      55      60
151 Val Pro Pro Thr Ile Arg Ser Ser Arg Thr Arg Pro His Leu Thr Ser
152 65      70      75      80

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154 Pro Pro Val Gln Pro Thr Trp Ser Ser Ala Ala His Leu Arg Ile Leu
155                      85                      90                      95
157 Gln Ser Ile Ile Val Gln Leu Val Gly Thr Leu Thr Thr Gly Ala Lys
158                      100                      105                      110
160 Ala Pro Leu Ser Gln Pro Ser Gln Pro Lys Arg His Pro
161                      115                      120                      125
163 <210> SEQ ID NO: 6
164 <211> LENGTH: 345
165 <212> TYPE: DNA
166 <213> ORGANISM: Mus sp.
168 <400> SEQUENCE: 6
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171 tcctgcaaga cttctggata cacattcaact gaatatacca tacactgggt gaagcagagc      120
173 catggaaga gccttgagtg gattggaaac atcaatccta acaatgggtg taccacctac      180
175 aatcagaagt tcgaggacaa ggccacattg actgtagaca agtcctccag tacagcctac      240
177 atggagctcc gcagcctaac atctgaggat tctgcagtct attattgtgc agctggttgg      300
179 aactttgact actggggcca aggcaccact ctcacagtct cctca                      345
182 <210> SEQ ID NO: 7
183 <211> LENGTH: 345
184 <212> TYPE: DNA
185 <213> ORGANISM: Mus sp.
187 <400> SEQUENCE: 7
188 tgaggagact gtgagagtgg tgccttggcc ccagtagtca aagttccaac cagctgcaca      60
190 ataatagact gcagaatcct cagatgttag gctgcggagc tccatgtagg ctgtactgga      120
192 ggacttgtct acagtcaatg tggccttgtc ctcgaacttc tgattgtagg tggtagcacc      180
194 attgttagga ttgatgtttc caatccactc aaggctcttt ccatggtctt gttcacccca      240
196 gtgtatggta tattcagtga atgtgtatcc agaagtcttg caggatatcc tcaactgaagt      300
198 ccaggcttc accagttcag gtccagactg ttgcagctgg acctc                      345
201 <210> SEQ ID NO: 8
202 <211> LENGTH: 115
203 <212> TYPE: PRT
204 <213> ORGANISM: Mus sp.
206 <400> SEQUENCE: 8
208 Glu Val Gln Leu Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Thr
209 1                      5                      10                      15
211 Ser Val Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Glu Tyr
212                      20                      25                      30
214 Thr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
215                      35                      40                      45
217 Gly Asn Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Lys Phe
218 50                      55                      60
220 Glu Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
221 65                      70                      75                      80
223 Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
224                      85                      90                      95
226 Ala Ala Gly Trp Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
227                      100                      105                      110
229 Val Ser Ser
230                      115

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232 <210> SEQ ID NO: 9
233 <211> LENGTH: 363
234 <212> TYPE: DNA
235 <213> ORGANISM: Mus sp.
237 <400> SEQUENCE: 9
238 ttatatggag ctgatgggaa cattgtaatg acccaatctc ccaaatccat gtccatgtca      60
240 gtaggagaga gggtcacctt gacctgcaag gccagtgaga atgtggttac ttatgtttcc      120
242 tggatcaaac agaaaccaga gcagtctcct aaactgctga tatacggggc atccaaccgg      180
244 tacactgggg tccccgatcg cttcacaggc agtggatctg caacagattt cactctgacc      240
246 atcagcagtg tgcaggctga agaccttgca gattatcact gtggacaggg ttacagctat      300
248 ccgtacacgt tcggaggggg gaccaagctg gaaataaaac gggctgatgc tgcaccaact      360
250 gta                                                                    363
253 <210> SEQ ID NO: 10
254 <211> LENGTH: 363
255 <212> TYPE: DNA
256 <213> ORGANISM: Mus sp.
258 <400> SEQUENCE: 10
259 tacagttggt gcagcatcag cccgttttat ttccagcttg gtccccctc cgaacgtgta      60
261 cggatagctg taaccctgtc cacagtgata atctgcaagg tcttcagcct gcacactgct      120
263 gatggtcaga gtgaaatctg ttgcagatcc actgcctgtg aagcgatcgg ggaccccagt      180
265 gtaccggttg gatgccccgt atatcagcag tttaggagac tgctctggtt tctgttgata      240
267 ccaggaaaca taagtaacca cattctcact ggccttgcat gtcaagggtga cctctctctc      300
269 tactgacatg gacatggatt tgggagattg ggtcattaca atgttcccat cagctccata      360
271 taa                                                                    363
274 <210> SEQ ID NO: 11
275 <211> LENGTH: 121
276 <212> TYPE: PRT
277 <213> ORGANISM: Mus sp.
279 <400> SEQUENCE: 11
281 Leu Tyr Gly Ala Asp Gly Asn Ile Val Met Thr Gln Ser Pro Lys Ser
282 1          5          10          15
284 Met Ser Met Ser Val Gly Glu Arg Val Thr Leu Thr Cys Lys Ala Ser
285          20          25          30
287 Glu Asn Val Val Thr Tyr Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln
288          35          40          45
290 Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val
291          50          55          60
293 Pro Asp Arg Phe Thr Gly Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr
294 65          70          75          80
296 Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln
297          85          90          95
299 Gly Tyr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
300          100         105         110
302 Lys Arg Ala Asp Ala Ala Pro Thr Val
303          115         120
305 <210> SEQ ID NO: 12
306 <211> LENGTH: 114
307 <212> TYPE: PRT
308 <213> ORGANISM: Mus sp.

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310 <400> SEQUENCE: 12

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312 Tyr Met Glu Leu Met Gly Thr Leu Pro Asn Leu Pro Asn Pro Cys Pro
313 1 5 10 15
315 Cys Gln Glu Arg Gly Ser Pro Pro Ala Arg Pro Val Arg Met Trp Leu
316 20 25 30
318 Leu Met Phe Pro Gly Ile Asn Arg Asn Gln Ser Ser Leu Leu Asn Cys
319 35 40 45
321 Tyr Thr Gly His Pro Thr Gly Thr Leu Gly Ser Pro Ile Ala Ser Gln
322 50 55 60
324 Ala Val Asp Leu Gln Gln Ile Ser Leu Pro Ser Ala Val Cys Arg Leu
325 65 70 75 80
327 Lys Thr Leu Gln Ile Ile Thr Val Asp Arg Val Thr Ala Ile Arg Thr
328 85 90 95
330 Arg Ser Glu Gly Gly Pro Ser Trp Lys Asn Gly Leu Met Leu His Gln
331 100 105 110

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333 Leu Tyr

336 <210> SEQ ID NO: 13

337 <211> LENGTH: 116

338 <212> TYPE: PRT

339 <213> ORGANISM: Mus sp.

341 <400> SEQUENCE: 13

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343 Ile Ile Trp Ser Trp Glu His Cys Asn Asp Pro Ile Ser Gln Ile His
344 1 5 10 15
346 Val His Val Ser Arg Arg Glu Gly His Leu Asp Leu Gln Gly Gln Glu
347 20 25 30
349 Cys Gly Tyr Leu Cys Phe Leu Val Ser Thr Glu Thr Arg Ala Val Ser
350 35 40 45
352 Thr Ala Asp Ile Arg Gly Ile Gln Pro Val His Trp Gly Pro Arg Ser
353 50 55 60
355 Leu His Arg Gln Trp Ile Cys Asn Arg Phe His Ser Asp His Gln Gln
356 65 70 75 80
358 Cys Ala Gly Arg Pro Cys Arg Leu Ser Leu Trp Thr Gly Leu Gln Leu
359 85 90 95
361 Ser Val His Val Arg Arg Gly Asp Gln Ala Gly Asn Lys Thr Gly Cys
362 100 105 110

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364 Cys Thr Asn Cys

365 115

367 <210> SEQ ID NO: 14

368 <211> LENGTH: 321

369 <212> TYPE: DNA

370 <213> ORGANISM: Mus sp.

372 <400> SEQUENCE: 14

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373 aacattgtaa tgacccaatc tcccaaatcc atgtccatgt cagtaggaga gagggtcacc 60
375 ttgacctgca aggccagtga gaatgtggtt acttatgttt cctggatatca acagaaacca 120
377 gagcagtcctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180
379 cgcttcacag gcagtggatc tgcaacagat ttactctga ccatacagcag tgtgcaggct 240
381 gaagaccttg cagattatca ctgtggacag gggtacagct atccgtacac gttcggaggg 300
383 gggaccaagc tggaaataaa a 321
386 <210> SEQ ID NO: 15

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VERIFICATION SUMMARY

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